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APR 06 2001

TECH CENTER 1600/2900

RAW SEQUENCE LISTING
PATENT APPLICATION: US/09/581,742

DATE: 03/28/2001
TIME: 17:53:46

Input Set : A:\P1548R1-US.txt
Output Set: N:\CRF3\03282001\I581742.raw

ENTERED

3 <110> APPLICANT: de Sauvage, Frederic J.
4 Gurney, Austin
5 Murone, Maximilien
6 Rosenthal, Arnon
7 Stone, Donna M.
8 Wood, William I.
10 <120> TITLE OF INVENTION: Human Suppressor of Fused
12 <130> FILE REFERENCE: P1548R1-US
C--> 14 <140> CURRENT APPLICATION NUMBER: US/09/581,742
C--> 14 <141> CURRENT FILING DATE: 2000-06-16
14 <150> PRIOR APPLICATION NUMBER: US 60/123,090
15 <151> PRIOR FILING DATE: 1999-03-05
17 <150> PRIOR APPLICATION NUMBER: US 60/135,736
18 <151> PRIOR FILING DATE: 1999-05-25
20 <150> PRIOR APPLICATION NUMBER: PCT/US00/05746
21 <151> PRIOR FILING DATE: 2000-03-02
23 <160> NUMBER OF SEQ ID NOS: 10
25 <210> SEQ ID NO: 1
26 <211> LENGTH: 1760
27 <212> TYPE: DNA
28 <213> ORGANISM: Homo sapiens
30 <400> SEQUENCE: 1
31 cccgctggcc cgctcagtgc cccccgctg tttgccctct ccagttcccc 50
33 cagtgcctgc cctacgcacc ccatggcgcg agctgcggcc tagcggcgcc 100
35 cccggcccca cgcgcgcccc ggcctctggc ccgactgcc ccccgccctt 150
37 cgcttcgctc ttcccccccg gactgcacgc catctacgga gagtgcggcc 200
39 gcctttaccc tgaccagccg aaccgcctcc aggttacgc tatcgtcaag 250
41 tactggttgg gtggcccaga ccccttgac tatgttagca tgtacaggaa 300
43 tgtggggagc ccttctgcta acatccccga gcaactggac tacatcagct 350
45 tcggcctgag tgatctctat ggtgacaaca gagtccatga gtttacagga 400
47 acagatggac ctagtgggtt tggctttgag ttgaccttc gtctgaagag 450
49 agaaactggg gagtctgccc caccaacatg gcccgagag ttaatgcagg 500
51 gcttggcacg atacgtgttc cagtcagaga acaccttctg cagtggggac 550
53 catgtgtcct ggcacagccc ttgggataac agtgagtcaa gaattcagca 600
55 catgctgctg acagaggacc cacagatgca gcccgtagc acacctttg 650
57 gggtagttac ctctctccag atcgttgggtg tctgcactga agagctacac 700
59 tcagcccagc agtggaacgg gcagggcatc ctggagctgc tgcggacagt 750
61 gcctattgct ggcggccctt ggctgataac tgacatgcgg aggggagaga 800
63 ccatatttga gatcgatcca cacctgcaag agagagttga caaaggcatc 850
65 gagacagatg gctccaacct gagtgggtgc agtgccaagt gtgcctggga 900
67 tgacctgagc cggcccccgg aggatgacga ggacagccgg agcatctgca 950
69 tcggcacaca gccccggcga ctctctggca aagacacaga gcagatccgg 1000
71 gagacctga ggagaggact cgagatcaac agcaaaccctg tccttccacc 1050
73 aatcaacctc cagcggcaga atggcctcgc ccacgaccgg gccccgagcc 1100
75 gcaaagacag cctggaaaag gacagctcca cggccatcat tccccatgag 1150
77 ctgattcgca cgcggcagct tgagagcgta catctgaaat tcaaccagga 1200
79 gtccggagcc ctcattctc tctgcctaag gggcaggctc ctgcatggac 1250

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81  ggcaactttac atataaaagt atcacaggtg acatggccat cacgtttgtc 1300
83  tccacgggag  tggaaggcgc ctttgccact gaggagcatc cttacgcggc 1350
85  tcatggaccc  tggttacaac  totgaacct  tctcgggagc  tctgccctcc 1400
87  cgtcctggaa  cgtcttttctg ccttgaggag agggtagtca gcatctccaa 1450
89  ttttcagcag  ctcaagaacc  ttggccccc  caggacttcg  cagatgtcac 1500
91  attgcccctc  agtcccctga  atgcccctcg  gacccaaccc  caattcccca 1550
93  agcccctgac  cccctagctg  ccgggggttc  cactcccagt  gccacaaccc 1600
95  cctcacctcc  cctggcagcc  cctcagcgag  cctgaggccc  agcacccgct 1650
97  ggctccccag  cacatgggtc  cctcccatgg  gctgttgccc  agggaaccgg 1700
99  ggcgcggtgg  gaacgagctg  ctggcctcgg  catgtttcaa  taaagttgct 1750
101  gtgctgggag 1760
103 <210> SEQ ID NO: 2
104 <211> LENGTH: 431
105 <212> TYPE: PRT
106 <213> ORGANISM: Homo sapiens
108 <400> SEQUENCE: 2
109  Met Ala Glu Leu Arg Pro Ser Gly Ala Pro Gly Pro Thr Ala Pro
110    1          5          10          15
112  Pro Ala Pro Gly Pro Thr Ala Pro Pro Ala Phe Ala Ser Leu Phe
113          20          25          30
115  Pro Pro Gly Leu His Ala Ile Tyr Gly Glu Cys Arg Arg Leu Tyr
116          35          40          45
118  Pro Asp Gln Pro Asn Pro Leu Gln Val Thr Ala Ile Val Lys Tyr
119          50          55          60
121  Trp Leu Gly Gly Pro Asp Pro Leu Asp Tyr Val Ser Met Tyr Arg
122          65          70          75
124  Asn Val Gly Ser Pro Ser Ala Asn Ile Pro Glu His Trp His Tyr
125          80          85          90
127  Ile Ser Phe Gly Leu Ser Asp Leu Tyr Gly Asp Asn Arg Val His
128          95          100         105
130  Glu Phe Thr Gly Thr Asp Gly Pro Ser Gly Phe Gly Phe Glu Leu
131          110         115         120
133  Thr Phe Arg Leu Lys Arg Glu Thr Gly Glu Ser Ala Pro Pro Thr
134          125         130         135
136  Trp Pro Ala Glu Leu Met Gln Gly Leu Ala Arg Tyr Val Phe Gln
137          140         145         150
139  Ser Glu Asn Thr Phe Cys Ser Gly Asp His Val Ser Trp His Ser
140          155         160         165
142  Pro Leu Asp Asn Ser Glu Ser Arg Ile Gln His Met Leu Leu Thr
143          170         175         180
145  Glu Asp Pro Gln Met Gln Pro Val Gln Thr Pro Phe Gly Val Val
146          185         190         195
148  Thr Phe Leu Gln Ile Val Gly Val Cys Thr Glu Glu Leu His Ser
149          200         205         210
151  Ala Gln Gln Trp Asn Gly Gln Gly Ile Leu Glu Leu Leu Arg Thr
152          215         220         225
154  Val Pro Ile Ala Gly Gly Pro Trp Leu Ile Thr Asp Met Arg Arg
155          230         235         240
157  Gly Glu Thr Ile Phe Glu Ile Asp Pro His Leu Gln Glu Arg Val

```

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```

158           245           250           255
160 Asp Lys Gly Ile Glu Thr Asp Gly Ser Asn Leu Ser Gly Val Ser
161           260           265           270
163 Ala Lys Cys Ala Trp Asp Asp Leu Ser Arg Pro Pro Glu Asp Asp
164           275           280           285
166 Glu Asp Ser Arg Ser Ile Cys Ile Gly Thr Gln Pro Arg Arg Leu
167           290           295           300
169 Ser Gly Lys Asp Thr Glu Gln Ile Arg Glu Thr Leu Arg Arg Gly
170           305           310           315
172 Leu Glu Ile Asn Ser Lys Pro Val Leu Pro Pro Ile Asn Pro Gln
173           320           325           330
175 Arg Gln Asn Gly Leu Ala His Asp Arg Ala Pro Ser Arg Lys Asp
176           335           340           345
178 Ser Leu Glu Ser Asp Ser Ser Thr Ala Ile Ile Pro His Glu Leu
179           350           355           360
181 Ile Arg Thr Arg Gln Leu Glu Ser Val His Leu Lys Phe Asn Gln
182           365           370           375
184 Glu Ser Gly Ala Leu Ile Pro Leu Cys Leu Arg Gly Arg Leu Leu
185           380           385           390
187 His Gly Arg His Phe Thr Tyr Lys Ser Ile Thr Gly Asp Met Ala
188           395           400           405
190 Ile Thr Phe Val Ser Thr Gly Val Glu Gly Ala Phe Ala Thr Glu
191           410           415           420
193 Glu His Pro Tyr Ala Ala His Gly Pro Trp Leu
194           425           430

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196 <210> SEQ ID NO: 3
197 <211> LENGTH: 346
198 <212> TYPE: DNA
199 <213> ORGANISM: Artificial sequence
201 <220> FEATURE:
202 <223> OTHER INFORMATION: consensus DNA used to isolate DNA 33454
204 <220> FEATURE:
205 <221> NAME/KEY: unsure
206 <222> LOCATION: 8, 28, 39, 54-55, 65, 68, 74, 80, 90, 125, 130
207 <223> OTHER INFORMATION: unknown base
209 <400> SEQUENCE: 3

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W--> 210 ggactgcntg ccatagcggt ttcccgcgtc ccaccgcgnc cccggcccat 50
W--> 212 gccnnactgc cccnccgnc ttañcatctñ tctttccan gggactgcac 100
W--> 214 gccatctacg gagagtgcg cgcñtttan ccttaccagc cgaaccgcgt 150
216 ccaggttacc gctatcgta agtactggtt ggggtgcccc gacccttgg 200
218 actatgttag catgtacagg aatgtgggga gcccttctgc taacatcccc 250
220 gagcactggc actacatcag cttcggcctg agtgatctct atggtgacaa 300
222 cagagtccat gaagtttaca ggaacagatg gacctagtgg ttttgt 346
224 <210> SEQ ID NO: 4
225 <211> LENGTH: 468
226 <212> TYPE: PRT
227 <213> ORGANISM: Drosophila Melanogaster
229 <400> SEQUENCE: 4
230 Met Ala Glu Ala Asn Leu Asp Lys Lys Pro Glu Val Lys Pro Pro

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231	1	5	10	15
233	Pro Gly Leu Lys Ala Ile Ile Asp His Leu Gly Gln Val Tyr Pro			
234		20	25	30
236	Asn Gln Pro Asn Pro Leu Gln Val Thr Thr Leu Leu Lys Tyr Trp			
237		35	40	45
239	Leu Gly Gly Gln Asp Pro Leu Asp Tyr Ile Ser Met Tyr Lys Phe			
240		50	55	60
242	Pro Gly Asp Val Asp Arg Asn Val Pro Pro His Trp His Tyr Ile			
243		65	70	75
245	Ser Phe Gly Leu Ser Asp Leu His Gly Asp Glu Arg Val His Leu			
246		80	85	90
248	Arg Glu Glu Gly Val Thr Arg Ser Gly Met Gly Phe Glu Leu Thr			
249		95	100	105
251	Phe Arg Leu Ala Lys Thr Glu Ile Glu Leu Lys Gln Gln Ile Glu			
252		110	115	120
254	Asn Pro Glu Lys Pro Gln Arg Ala Pro Thr Trp Pro Ala Asn Leu			
255		125	130	135
257	Leu Gln Ala Ile Gly Arg Tyr Cys Phe Gln Thr Gly Asn Gly Leu			
258		140	145	150
260	Cys Phe Gly Asp Asn Ile Pro Trp Arg Lys Ser Leu Asp Gly Ser			
261		155	160	165
263	Thr Thr Ser Lys Leu Gln Asn Leu Leu Val Ala Gln Asp Pro Gln			
264		170	175	180
266	Leu Gly Cys Ile Asp Thr Pro Thr Gly Thr Val Asp Phe Cys Gln			
267		185	190	195
269	Ile Val Gly Val Phe Asp Asp Glu Leu Glu Gln Ala Ser Arg Trp			
270		200	205	210
272	Asn Gly Arg Gly Val Leu Asn Phe Leu Arg Gln Asp Met Gln Thr			
273		215	220	225
275	Gly Gly Asp Trp Leu Val Thr Asn Met Asp Arg Gln Met Ser Val			
276		230	235	240
278	Phe Glu Leu Phe Pro Glu Thr Leu Leu Asn Leu Gln Asp Asp Leu			
279		245	250	255
281	Glu Lys Gln Gly Ser Asp Leu Ala Gly Val Asn Ala Asp Phe Ser			
282		260	265	270
284	Phe Arg Glu Leu Lys Pro Thr Lys Glu Val Lys Glu Glu Val Asp			
285		275	280	285
287	Phe Gln Ala Leu Ser Glu Lys Cys Ala Asn Asp Glu Asn Asn Arg			
288		290	295	300
290	Gln Leu Thr Asp Thr Gln Met Lys Arg Glu Glu Pro Ser Phe Pro			
291		305	310	315
293	Gln Ser Met Ser Met Ser Ser Asn Ser Leu His Lys Ser Cys Pro			
294		320	325	330
296	Leu Asp Phe Gln Ala Gln Ala Pro Asn Cys Ile Ser Leu Asp Gly			
297		335	340	345
299	Ile Glu Ile Thr Leu Ala Pro Gly Val Ala Lys Tyr Leu Leu Leu			
300		350	355	360
302	Ala Ile Lys Asp Arg Ile Arg His Gly Arg His Phe Thr Phe Lys			
303		365	370	375

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```

305  Ala Gln His Leu Ala Leu Thr Leu Val Ala Glu Ser Val Thr Gly
306                      380                      385                      390
308  Ser Ala Val Thr Val Asn Glu Pro Tyr Gly Val Leu Gly Tyr Trp
309                      395                      400                      405
311  Ile Gln Val Leu Ile Pro Asp Glu Leu Val Pro Arg Leu Met Glu
312                      410                      415                      420
314  Asp Phe Cys Ser Ala Gly Leu Asp Glu Lys Cys Glu Pro Lys Glu
315                      425                      430                      435
317  Arg Leu Glu Leu Glu Trp Pro Asp Lys Asn Leu Lys Leu Ile Ile
318                      440                      445                      450
320  Asp Gln Pro Glu Pro Val Leu Pro Met Ser Leu Asp Ala Ala Pro
321                      455                      460                      465
323  Leu Lys Met
326 <210> SEQ ID NO: 5
327 <211> LENGTH: 275
328 <212> TYPE: DNA
329 <213> ORGANISM: Mus musculus
331 <400> SEQUENCE: 5
332  gagagtgtcg cgcctctac cctgaccagc cgaacccgct ccaggttacc 50
334  gctatcgtca agtactggtt ggggtggtccg gacccttgg actatgttag 100
336  catgtacagg aacatgggga gtccttctgc caacatccct gagcactggc 150
338  actacatcag ctttggcctg agtgatctct atggtgacaa cagagtccat 200
340  gagtttacag gaacagacgg accaagtgga tttggctttg agttgacggt 250
342  tcgtctgaag agagaaactg gggag 275
344 <210> SEQ ID NO: 6
345 <211> LENGTH: 23
346 <212> TYPE: DNA
347 <213> ORGANISM: Artificial sequence
349 <220> FEATURE:
350 <223> OTHER INFORMATION: forward PCR cloning primer
352 <400> SEQUENCE: 6
353  cagccgaacc cgctccaggt tac 23
355 <210> SEQ ID NO: 7
356 <211> LENGTH: 25
357 <212> TYPE: DNA
358 <213> ORGANISM: Artificial sequence
360 <220> FEATURE:
361 <223> OTHER INFORMATION: reverse PCR cloning primer
363 <400> SEQUENCE: 7
364  catggactct gttgtcacca tagag 25
366 <210> SEQ ID NO: 8
367 <211> LENGTH: 40
368 <212> TYPE: DNA
369 <213> ORGANISM: Artificial sequence
371 <220> FEATURE:
372 <223> OTHER INFORMATION: hybridization probe
374 <400> SEQUENCE: 8
375  gagcactggc actacatcag ctttggcctg agtgatctct 40
377 <210> SEQ ID NO: 9

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VERIFICATION SUMMARY
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L:14 M:270 C: Current Application Number differs, Replaced Current Application No
L:14 M:271 C: Current Filing Date differs, Replaced Current Filing Date
L:210 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:3
L:212 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:3
L:214 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:3